

FIG. 1A

Input file Fbh56919FL2.seq
Sequence length 3003

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TCGCGCACGAGCTGCTGGGGGGGACTCTTTCTGAGGTTACTGTGGAGCACCCAAAGTCTGTGAGCCTCTGGCGGTGC
13
AAACAGGCACCCAGAGAACACGACCTTGCTTATTCCACCCAGAGCTGGAGTGTCTTCTCCAGAGTCTCCATCAGCTT
39
TGCTAATCGACTGATTGGAAATAATCTCTCAAAACACACCAAGTCAAGGATACAGCAGCAGCGGCTCCCTCTGTGTAT
33
GGACATTCCTGCACCCGAAACTGATAGCTGAGTCTGCTGAAAGTTTATGTTATGAAAGAAAGAACTTTTCATCCACGACAT
99
M D E S A L T L G T I D V
GATTTGGGAATTACACTTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GGT ACA ATA GAT GTT
39
S Y L P H S S E Y S V G R C K H T S E E
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AAG CAC ACA AGT GAG GAA
53
W G E C G F R P T V F R S A T L K W K E
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA
159
S L M S R K R P P F V G R C C Y S C T P Q
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TGT TAC TCC TGC ACT CCC CAG
73
S W D K F F N P S I P S L G L R N V I Y
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT
93
I N E T H T R H R G W L A R R L S Y V L
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT
113
F I Q E R D V H K G M F A T N V T E N V
TTT ATT CAA GAG CGA GAT GTC CAT AAG GGC ATG TTT GCC ACC AAT GTG ACT GAA AAT GTG
133
399

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FIG. 1B

| | |
|---|-----|
| L N S S R V Q E A I A E V A A E L N P D | 153 |
| CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT | 459 |
| G S A Q Q Q S K A V N K V K K K A K R I | 173 |
| GGT TCT GCC CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT | 519 |
| L Q E M V A T V S P A M I R L T G W V L | 193 |
| CTT CAA GAA ATG GTT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GGG TGG GTG CTG | 579 |
| L K L F N S F F W N I Q I H K G Q L E M | 213 |
| CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG | 639 |
| V K A A T E T N L P L L F L P V H R S H | 233 |
| GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT | 699 |
| I D Y L L L T F I L F C H N I K A P Y I | 253 |
| ATT GAC TAT CTG CTG CTC ACT TTC ATT TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT | 759 |
| A S G N N L N I P I F S T L I H K L G G | 273 |
| GCT TCA GGC AAT AAT CTC AAC ATC CCA ATC TTC AGT ACC TTG ATC CAT AAG CTT GGG GGC | 819 |
| F F I R R R L D E T P D G R K D V L Y R | 293 |
| TTC TTC ATA CGA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA | 879 |
| A L L H G H I V E L L R Q Q Q F L E I F | 313 |
| GCT TTG CTC CAT GGG CAT ATA GTT GAA TTA CTT CGA CAG CAG CAA TTC TTG GAG ATC TTC | 939 |
| L E G T R S R S G K T S C A R A G L L S | 333 |
| CTG GAA GGC ACA CGT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA | 999 |

FIG. 1C

V V V D T L S T N V I P D I L I I P V G 353
 GTT GTG GTA GAT ACT CTG TCT ACC AAT GTC ATC CCA GAC ATC TTG ATA ATA CCT GTT GGA 1059

 I S Y D R I I E G H Y N G E Q L G K P K 373
 ATC TCC TAT GAT CGC ATT ATC GAA GGT CAC TAC AAT GGT GAA CAA CTG GGC AAA CCT AAG 1119

 K N E S L W S V A R G V I R M L R K N Y 393
 AAG AAT GAG AGC CTG TGG AGT GTA GCA AGA GGT GTT ATT AGA ATG TTA CGA AAA AAC TAT 1179

 G C V R V D F A Q P F S L K E Y L E S Q 413
 GGT TGT GTC CGA GTG GAT TTT GCA CAG CCA TTT TCC TTA AAG GAA TAT TTA GAA AGC CAA 1239

 S Q K P V S A L L S L E Q A L L P A I L 433
 AGT CAG AAA CCG GTG TCT GCT CTA CTT TCC CTG GAG CAA GCG TTG TTA CCA GCT ATA CTT 1299

 P S R P S D A A D E G R D T S I N E S R 453
 CCT TCA AGA CCC AGT GAT GCT GAT GAA GGT AGA GAC ACG TCC ATT AAT GAG TCC AGA 1359

 N A T D E S L R R R L I A N L A E H I L 473
 AAT GCA ACA GAT GAA TCC CTA CGA AGG AGG TTG ATT GCA AAT CTG GCT GAG CAT ATT CTA 1419

 F T A S K S C A I M S T H I V A C L L L 493
 TTC ACT GCT AGC AAG TCC TGT GCC ATT ATG TCC ACA CAC ATT GTG GCT TGC CTG CTC CTC 1479

 Y R H R Q G I D L S T L V E D F F V M K 513
 TAC AGA CAC AGG CAG GGA ATT GAT CTC TCC ACA TTG GTC GAA GAC TTC TTT GTG ATG AAA 1539

 E E V L A R D F D L G F S G N S E D V V 533
 GAG GAA GTC CTG GCT CGT GAT TTT GAC CTG GGG TTC TCA GGA AAT TCA GAA GAT GTA GTA 1599

FIG. 1D

M H A I Q L L G N C V T I T H T S R N D 553
 ATG CAT GCC ATA CAG CTG CTG GGA AAT TGT GTC ACA ATC ACC CAC ACT AGC AGG AAC GAT 1659
 E F I T P S T V P S V F E L N F Y S 573
 GAG TTT TTT ATC ACC CCC AGC ACA ACT GTC CCA TCA GTC TTC GAA CTC AAC TTC TAC AGC 1719
 N G V L H V F I M E A I I A C S L Y A V 593
 AAT GGG GTA CTT CAT GTC TTT ATC ATG GAG GCC ATC ATA GCT TGC AGC CTT TAT GCA GTT 1779
 L N K R G L G G P T S T P P N L I S Q E 613
 CTG AAC AAG AGG GGA CTG GGG GGT CCC ACT AGC ACC CCA CCT AAC CTG ATC AGC CAG GAG 1839
 Q L V R K A A S L C Y L L S N E G T I S 633
 CAG CTG GTG CGG AAG GCG GCC AGC CTG TGC TGC TAC CTT CTC TCC AAT GAA GGC ACC ATC TCA 1899
 L P C Q T F Y Q V C H E T V G K F I Q Y 653
 CTG CCT TGC CAG ACA TTT TAC CAA GTC TGC CAT GAA ACA GTA GGA AAG TTT ATC CAG TAT 1959
 G I L T V A E H D D Q E D I S P S L A E 673
 GGC ATT CTT ACA CTG GCA GAG CAC GAT GAC CAG GAA GAT ATC AGT CCT AGT CTT GCT GAG 2019
 Q Q W D K K L P E P L S W R S D E E D E 693
 CAG CAG TGG GAC AAG AAG CTT CCA GAA CCT TTG TCT TGG AGA AGT GAT GAA GAA GAT GAA 2079
 D S D F G E E Q R D C Y L K V S Q S K E 713
 GAC AGT GAC TTT GGG GAG GAA CAG CGA GAT TGC TAC CTG AAG GTG AGC CAA TCC AAG GAG 2139
 H Q Q F I T F L Q R L L G P L L E A Y S 733
 CAC CAG CAG TTT ATC ACC TTC TTA CAG AGA CTC CTT GGG CCT TTG CTG GAG GCC TAC AGC 2199

FIG. 1E

| | | | | | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| S | A | A | I | F | V | H | N | F | S | G | P | V | P | E | P | E | Y | L | Q | 753 |
| TCT | GCT | GCC | ATC | TTT | GTT | CAC | AAC | TTC | AGT | GGT | CCT | GTT | CCA | GAA | CCT | GAG | TAT | CTG | CAA | 2259 |
| K | L | H | K | Y | L | I | T | R | T | E | R | N | V | A | V | Y | A | E | S | 773 |
| AAG | TTG | CAC | AAA | TAC | CTA | ATA | ACC | AGA | ACA | GAA | AGA | AAT | GTT | GCA | GTA | TAT | GCT | GAG | AGT | 2319 |
| A | T | Y | C | L | V | K | N | A | V | K | M | F | K | D | I | G | V | F | K | 793 |
| GCC | ACA | TAT | TGT | CTT | GTG | AAG | AAT | GCT | GTG | AAA | ATG | TTT | AAG | GAT | ATT | GGG | GTT | TTC | AAG | 2379 |
| E | T | K | Q | K | R | V | S | V | L | E | L | S | S | T | F | L | P | Q | C | 813 |
| GAG | ACC | AAA | CAA | AAG | AGA | GTG | TCT | GTT | TTA | GAA | CTG | AGC | AGC | ACT | TTT | CTA | CCT | CAA | TGC | 2459 |
| N | R | Q | K | L | L | E | Y | I | L | S | F | V | V | L | * | | | | | 829 |
| AAC | CGA | CAA | AAA | CTT | CTA | GAA | TAT | ATT | CTG | AGT | TTT | GTG | GTG | CTG | TAG | | | | | 2487 |
| GTAACGTGTGGCACTGCTGGCAATGAAGGTCAATGAGATGAGTTCCTTTGTAGTACCAGCTTCTGTGCTCAAGAGTTTGA | | | | | | | | | | | | | | | | | | | | |
| AGGTGCCTTCGCAAGGGTCAGGCCCTGCCCTGTNCCGAAGTGATCTCTCTGGAGACAAAGTGCCTTCTNCCCTCATGGATC | | | | | | | | | | | | | | | | | | | | |
| TGAGATCTTCCACGCTTT | | | | | | | | | | | | | | | | | | | | |

FIG. 2

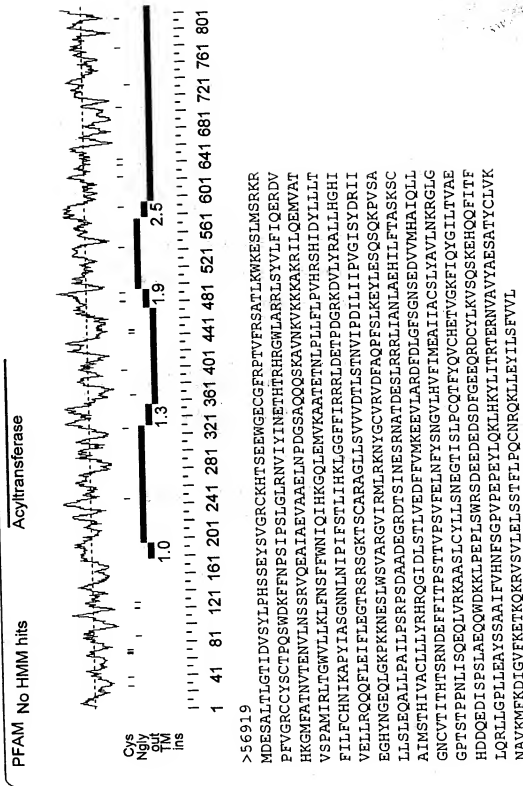


FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

 HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.21255.seq

Query: 56919

Scores for sequence family classification (score includes all domains):

| Model | Description | Score | E-value | N |
|-----------------|-----------------|-------|---------|-------|
| ----- | ----- | ----- | ----- | ----- |
| Acyltransferase | Acyltransferase | 126.1 | 6.4e-34 | 1 |

Parsed for domains:

| Model | Domain | seq-f | seq-t | hmm-f | hmm-t | score | E-value |
|-----------------|--------|-------|-------|-------|-------|-------|---------|
| ----- | ----- | ----- | ----- | ----- | ----- | ----- | ----- |
| Acyltransferase | 1/1 | 215 | 412 | 1 | 195 | 126.1 | 6.4e-34 |

FIG. 3B

Alignments of top-scoring domains:

Acyitransferase: domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34

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*->lenipkkgpaivsnHrSydlivlsaaiprggpwlrvrlvfiakke
+ +++++ p ++ + HcS++D+l+l ++l++++ ++ +ia ++
56919 215 KAAETNLPLELFPVHRSHIDYLLTLFILFCHN----IKAPYIASGN 257

llkvPllifGwlmrlagaifidRnnra.....kdalaaadelvrvlellrk
+l++P+ f++l+ ++g +fi+R+ ++++++kd l++a+ + + +ellr+
56919 258 NLNIPi-FSTLIHKLGFFIRRLDEtpdgrKDVLRYALLHGHIVELLRQ 306

grsvliFPEGTRsrsgellppfKkGia.....afrlAlkagvpiVPvviV
+ + iF EGTRsrsg++ + ++G+++ + + ++ ++ i+Pv+i
56919 307 QQFIEIFLEGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILLIPVGI- 354

sgteelepkneargklrlarkkpgvtvrvlppipld..pedikelaelr
s++ ++e +++++ + ++++++ v +++ +++++ +
56919 355 SYDRIIEGHNGEQ--LGKPKNESLWSVARGVIRMLFKNYGCVRVDFAQ 402

dilvqaleel<+
+ +++++ e+
56919 403 PFSLKEYLES 412

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FIG. 4A

| ProDom Matches ProDomId | Start | End | Description | Score |
|----------------------------|-------|-----|---|-------|
| View Prodom PD347660 | 1 | 55 | p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL | 250 |
| View Prodom PD087501 | 51 | 158 | p2001.1 (1) // AIP2-DLD1 | 77 |
| View Prodom PD353751 | 56 | 152 | p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL | 500 |
| View Prodom PD037846 | 128 | 259 | p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR MITOCHONDRION | 258 |
| View Prodom PD042466 | 259 | 590 | p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE MITOCHONDRION | 413 |
| View Prodom PD025192 | 462 | 649 | p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION | |

FIG. 4B

458

View Prodrom PD042027 465 673 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE
GLYCEROL-3-PHOSPHATE MEMBRANE
PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

80

View Prodrom PD042760 650 828 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE
PHOSPHOLIPID BIOSYNTHESIS PRECURSOR
TRANSMEMBRANE GLYCEROL-3-PHOSPHATE
GPAT MITOCHONDRION MITOCHONDRIAL

799

View Prodrom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
MITOCHONDRIAL
Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79
Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FTQYGILTVAEHDDQEDISPLAEQQWDKLPEPLSWRXXXXXXXXXXXXQDCYLKVS 709
FTQYGILTVAE DDQED+SP LAEQW+KLUPEPL+WR QDCYLKVS

Sbjct: 1 FTQYGILTVAEQQDDQEDVSPGLAEQQWNNKLPEPLNRSDEDEDSDFGEEQRDCYLKVS 60

Query: 710 QKHEHQOFTIFLQRLGPLELAYSSAAIFVNFSGPPEPEYLQKLHKYLITRERNVAV 769
Q+KHEHQOFTIFLQRLGPLELAYSSAAIFVNF GPYPE EYIQKLH+YLITRERNVAV

Sbjct: 61 QAKEHQOFTIFLQRLGPLELAYSSAAIFVNFSGPPEPEYLQKLHKYLITRERNVAV 120

Query: 770 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSTFLPQCNRQKLEYILSFVL 828
YAESATYCLVKNVAKMFKDIGVFKETKOKR SVLELS+TELPQCNRQKLEYILSFVL

Sbjct: 121 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSTFLPQCNRQKLEYILSFVL 179

FIG. 4C

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRIAL
 Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47
 Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSRRKPFVGRCCYSCPTQSQWDFNPSIPSLGRNVIIYNETHTRHGWLAARRLSYVLEI 115
 MSRRKPFVGRCCYSCPTQSQW++FFNPSPSLGRNVIIYNETHTRHGWLAARRLSY+LF+
 Sbjct: 1 MSRRKPFVGRCCYSCPTQSQWERFNPSPSLGRNVIIYNETHTRHGWLAARRLSYILFV 60

Query: 116 QERDVHKGMEFATNTVENVLNSSRVQEAIAEVAALNP 152
 QERDVHKGMEFAT+T+NVLNSSRVQEAIAEVAALNP
 Sbjct: 61 QERDVHKGMEFATITDNLNLSRVQEAIAEVAALNP 97

View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL
 BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT
 MITOCHONDRION
 Length = 194

Score = 458 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43
 Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RRLIANLAELHIFTASKSCAIMSTHIVACILLVNRHOGIDLSTLVEDFFVMKEEVLARDF 521
 R LI ++ EH++F S C+IMSTH+VACILL R R G+ STL ED + E++IA
 Sbjct: 3 RNLIRSIGEHVVFDSCMMCSIMSTHIVACILLITWRNGVHRSTLEEDCDWLCEKILAEGG 62

FIG. 4D

Query: 522 DL-CFSGNS---EDVVMHAIQLLGNVCVTITHTSRNDEFFITPSTVPSVFEINLYSNGVL 577
 D+ GFSG S +V +A +LLG+CVT+T RNDER+I+P +VPS EL +YSN V+
 Sbjct: 63 DIVFGSKTKGQIVKVIACELLGSCVTVDEDRDEFYISPKNSVPSFIELAYYSNVI 122

Query: 578 HVFTMEALIIACSLYAVLNKRGGLGFTSTPENLISQQLVVRKAASLCYLLSNEGTTISLPCQ 637
 F +++ITAC++Y++ NK GG NLISQQLV A SLC L E PCQ
 Sbjct: 123 CHEFALKSIIACTIYSLPNKTKNGGAGGLNLISQQLVEDALSLCDWLQYEFMECRQC 182

Query: 638 TFYQVCHETVGK 649
 T ++CH T+GK
 Sbjct: 183 TLRELCHNTLTK 194

View Prodom PD042466

>PD042466 p2001.1 (116) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE
 MITOCHONDRION
 Length = 299

Score = 413 (150.4 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 79/152 (51%), Positives = 108/152 (71%)

Query: 259 LNIPIFTSLIHLKGGFTIRRLDETDPGRKDVLYRALLGHIVELLRQQQLEIFLEIGTR 318
 L++PI ++L+ G FFIR D TP+G+ D LYRA+ H ++ +L+ + -E F+EGTR
 Sbjct: 2 LSPMFGSLLRRTGAFIRRSFDPTEPGKGQLYRAVFHEYVAQLISKYGNIEFFIEGTR 61

Query: 319 SRSGKTSARAGLLSVVVDTLTSTNVIPDILIPVGSYDRRIEGH-YNQEQLGKPKKNES 377
 SR+GK + GLLS+VV+ +PDIL++PV ISYDRRIEG+ Y E G PKK ES
 Sbjct: 62 SRTGKMLPFPKGLLSMVVVEAFIRGSVPDILLVPVSYDRRIEGNTYAHELRGAPKKES 121

FIG. 4E

Query: 378 LWSVARGVIRMLRKNYGCVRVDFAQPFSLKEY 409
 LW + RG + ML++NYG V VDF +P SL+EY
 Sbjct: 122 LWQFRGVARKLKNYGVYVDFGEPISLREY 153

Score = 64 (27.6 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 30/143 (20%), Positives = 59/143 (41%)

Query: 453 RNATDSLRRLRIANLAELHIFTASKSCAIMSTHIVACLLILYRHRQIGIDLSTL---VEDE 509
 RN + + +R + ++ + + ++ + +T +V+ LLL + L L ++D
 Sbjct: 160 RNTYNCAPKRLALQKMSFEVAVNRILQATPVTATGLVSALLITTRGTALTLDQLHHTLQDS 219

Query: 510 FVMKEEVLARDELDGFGSGNSEDVYVMAIQLL--GNCVTITHTSRNDSEFFITPSTTVPSVF 567
 E + S + V A L G+ VT + R ++I P + F
 Sbjct: 220 LDYLERKQSEVSTSAURLRSREGVRAAADALSGHPVTRVDSGREPVWYIAPDDEHAAAF 279

Query: 568 ELNFYNGVLHVFIEMAIACSL 590
 Y N V+H P+ +I+ +L
 Sbjct: 280 ----YRNSVIHAFLETSIVELAL 298

View Prodom PD037846

>PD037846 p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR
 MITOCHONDRION
 Length = 345

Score = 258 (95.9 bits), Expect = 3.4e-21, P = 3.4e-21
 Identities = 56/132 (42%), Positives = 79/132 (59%)

FIG. 4F

Query: 128 NVTENVLSSRVQEAIAEVAELNPDGSAQOQOQXXXXXXXXXXRIIQENMVAIVSPAMIR 187
 N+ +NVINS + I + A++ S IL EM T++ MIR
 Sbjct: 223 NLKKNVLNSEEIHYVIEQ-----EAKESSTSIDKVRREAREIIDEMSHLINMGWIR 273

Query: 188 LTGWILLKLFNGFFWNIQIHKGOLEWVKAATETNLP LLFLPVRHSHIDYLLLTFFILFCHN 247
 GWVL K+FN F I +++ Q+E +K ATE P+++LP HRSHIDYLL+FIL+ ++
 Sbjct: 274 FCGWLSKTFNRFSGICVNEEQIEKIKRATEQGHVPVILPSPHRSHIDYLLLSFILIYHD 333

Query: 248 IKAPYIASGNL 259
 IK P+IA+G NL
 Sbjct: 334 IKVPPIAAGWNL 345

View Prodrom PD347660

>PD347660 p2001.1 (2) PL5B(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRIAL
 Length = 55

Score = 250 (93.1 bits), Expect = 2.4e-20, P = 2.4e-20
 Identities = 43/55 (78%), Positives = 53/55 (96%)

Query: 1 MDESALTGLTIDVSYLPSPHSSEYSVGRCKTSEWGECCGFRPTVFRSATLKWKESL 55
 M+ES++T+GTIDVSYLP+SSEYS+GRCKT+E+W +CGF+PT FRSATLKWKESL
 Sbjct: 1 MEESSTVIGTIDVSYLPNSSEYSGLGRCKHTNEDWDVDCGFKPTFFRSATLKWKESL 55

FIG. 4G

View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE
 PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT
 Length = 345

Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAEHILFTASKSCAIMSTHIVACLLYHRHQGLDSTLVE--DFFVMKEEVLARDFD 522
 + +LA+ I+ + + + A+ ++ A LL ++ + L+E D ++ + D

Sbjct: 32 VNHAKQIMTHINDAAAVNPNLCATALLSTRQRALGEEQLIEQLDCYLKLRNVPYSTD 91

Query: 523 LGFSGNS-EDVVMHAIQ--LLGNCVTITHTSRNDEFFITPSTVPSELFNFYSNGVLHV 579
 ++ E ++ HA Q LLG VT+ + D + V + +Y N VLH+

Sbjct: 92 ATLPDHTPERLIEHAEQNNLLG--VTVEKDTLGLRLDRDNAV-----MTYRNNVLHL 145

Query: 580 FIMEAIIAC 588

F + A++AC

Sbjct: 146 FALPALVAC 154

Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 LNFYSGVLVHVFIMEAIIACSLYAVLNKRGGLGGFTSTFPNLSIQEQLVRKAASLCYLLSN 628
 + +Y N VLH+F + A++AC N+R IS++ L+R +L L

Sbjct: 135 MTYRNNVLHVFALPALVACCFKN--NRR-----ISRDLALREVVALYFFLQA 180

Query: 629 EGTISLPQCTFYQVCHETVGRKFIQYGLITVAEHDDQEDISPSLAE 673

E + + + +F++ G+L A + + + ++ + ++

Sbjct: 181 ELFLRWNEDELNDHIDOWINEFVRQGLLSAGNQEDDTLTRNTSQ 225

FIG. 4H

View Prodom PD087501

>PD087501 p2001.1 (1) // AIP2-DLD1
 Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994
 Identities = 31/114 (27%), Positives = 44/114 (38%)

Query: 51 WKES--LMSRRPFVGRCCYCTPQSWDKFNFSPSLGRNVIIYNETHTRHGWLAER 108
 W ES L+ RK F RCC P K + L N +H W
 Sbjct: 12 WNESEVLYDRSKTQARCC---PLQNKDIPSLQELTQNNKSVSKASHMHMYAWRTAE 67

Query: 109 LSYVLFIQERDVHKGMEATNVTVNLSSR---VQ-EATAEVAEELNPDGSAQQ 158
 +S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+
 Sbjct: 68 VSNLHLQEOEOKKGNKANKSNNSHVNSRNTVQPKNIEQGCADCGEAGAGOR 121

FIG. 5A

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|---------|------|---------------------------------|---------------------|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----------|---------------|---------------|-------------|---------------|
| | 10 | 20 | 30 | 40 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1 | MDESALT | LG | TIDVSYLPHSSEYSVGRCKHTSEEWGECGFR | | 56919.pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1 | MEESSVT | VG | TIDVSYLPSSEYSVGRCKHTSEEDWVDCGFK | | MouseGPAT.PRO | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1 | MEESSVT | IG | TIDVSYLPNSSEYSVGRCKHTNEDWVDCGFK | | RatGPAT.PRO | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 50 | 60 | 70 | 80 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 41 | PTVFR | SATL | KWKESLMSRKRP | FFVGRCCYCTPQSWDKFFN | 56919.pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 41 | PTFFRS | ATL | KWKESLMSRKRP | FFVGRCCYCTPQSWERFFN | MouseGPAT.PRO | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 41 | PTFFRS | ATL | KWKESLMSRKRP | FFVGRCCYCTPQSWERFFN | RatGPAT.PRO | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | 90 | 100 | 110 | 120 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 81 | PSIPSL | G | L | R | N | V | I | Y | I | N | E | T | H | T | R | H | R | G | L | A | R | R | L | S | Y | I | L | F | V | Q | E | R | D | V | | 56919.pro | | |
| 81 | PSIPSL | G | L | R | N | V | I | Y | I | N | E | T | H | T | R | H | R | G | L | A | R | R | L | S | Y | I | L | F | V | Q | E | R | D | V | | MouseGPAT.PRO | | |
| 81 | PSIPSL | G | L | R | N | V | I | Y | I | N | E | T | H | T | R | H | R | G | L | A | R | R | L | S | Y | I | L | F | V | Q | E | R | D | V | | RatGPAT.PRO | | |
| | 130 | 140 | 150 | 160 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 121 | HKGMF | A | T | S | I | T | D | N | V | L | N | S | S | R | V | Q | E | A | I | A | E | V | A | E | L | N | P | D | G | S | A | Q | Q | S | | 56919.pro | | |
| 121 | HKGMF | A | T | S | I | T | D | N | V | L | N | S | S | R | V | Q | E | A | I | A | E | V | A | E | L | N | P | D | G | S | A | Q | Q | S | | MouseGPAT.PRO | | |
| 121 | HKGMF | A | T | S | I | T | D | N | V | L | N | S | S | R | V | Q | E | A | I | A | E | V | A | E | L | N | P | D | G | S | A | Q | Q | S | | RatGPAT.PRO | | |
| | 170 | 180 | 190 | 200 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 161 | KAVNK | V | K | K | K | A | K | R | I | L | Q | E | M | V | A | T | V | S | P | A | M | I | R | L | T | G | W | V | L | L | K | L | F | N | S | F | | 56919.pro |
| 161 | KAIQK | V | K | R | K | A | K | R | I | L | Q | E | M | V | A | T | V | S | P | G | M | I | R | L | T | G | W | V | L | L | K | L | F | N | S | F | | MouseGPAT.PRO |
| 161 | KAIQK | V | K | R | K | A | K | R | I | L | Q | E | M | V | A | T | V | S | P | G | M | I | R | L | T | G | W | V | L | L | K | L | F | N | S | F | | RatGPAT.PRO |
| | 210 | 220 | 230 | 240 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 201 | FWNIQ | I | H | K | G | L | E | M | V | K | A | A | T | E | T | N | L | P | L | L | F | L | P | V | H | R | S | H | I | D | Y | L | L | L | | 56919.pro | | |
| 201 | FWNIQ | I | H | K | G | L | E | M | V | K | A | A | T | E | T | N | L | P | L | L | F | L | P | V | H | R | S | H | I | D | Y | L | L | L | | MouseGPAT.PRO | | |
| 201 | FWNIQ | I | H | K | G | L | E | M | V | K | A | A | T | E | T | N | L | P | L | L | F | L | P | V | H | R | S | H | I | D | Y | L | L | L | | RatGPAT.PRO | | |
| | 250 | 260 | 270 | 280 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 241 | FILFCH | N | I | K | A | P | Y | I | A | S | G | N | N | L | N | I | P | I | F | S | T | L | I | H | K | L | G | G | F | I | R | R | L | | 56919.pro | | | |
| 241 | FILFCH | N | I | K | A | P | Y | I | A | S | G | N | N | L | N | I | P | I | V | F | S | T | L | I | H | K | L | G | G | F | I | R | R | L | | MouseGPAT.PRO | | |
| 241 | FILFCH | N | I | K | A | P | Y | I | A | S | G | N | N | L | N | I | P | I | F | S | T | L | I | H | K | L | G | G | F | I | R | R | L | | RatGPAT.PRO | | | |
| | 290 | 300 | 310 | 320 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 281 | DETPD | G | R | K | D | I | L | Y | R | A | L | L | H | G | H | I | V | E | L | L | R | Q | Q | F | L | E | I | F | L | E | G | T | R | S | R | | 56919.pro | |
| 281 | DETPD | G | R | K | D | I | L | Y | R | A | L | L | H | G | H | V | E | L | L | R | Q | Q | F | L | E | I | F | L | E | G | T | R | S | R | | MouseGPAT.PRO | | |
| 281 | DETPD | G | R | K | D | I | L | Y | R | A | L | L | H | G | H | I | V | E | L | L | R | Q | Q | F | L | E | I | F | L | E | G | T | R | S | R | | RatGPAT.PRO | |
| | 330 | 340 | 350 | 360 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 321 | SGKTSC | A | R | A | G | L | L | S | V | V | V | D | T | L | S | N | V | I | P | D | I | L | I | P | V | G | I | S | Y | D | R | I | | 56919.pro | | | | |
| 321 | SGKTSC | A | R | A | G | V | L | S | V | V | N | T | L | S | S | N | T | I | P | D | I | L | V | I | P | V | G | I | S | Y | D | R | I | | MouseGPAT.PRO | | | |
| 321 | SGKTSC | A | R | A | G | L | L | S | V | V | V | D | T | L | S | S | N | T | I | P | D | I | L | V | I | P | V | G | I | S | Y | D | R | I | | RatGPAT.PRO | | |

FIG. 5B

| | | | | | |
|-----|---|-----|-----|-----|---------------|
| | 370 | 380 | 390 | 400 | |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGCVRVDF | | | | 56919.pro |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF | | | | MouseGPAT.PRO |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF | | | | RatGPAT.PRO |
| | 410 | 420 | 430 | 440 | |
| 401 | AQPFSLKEYLESQSQKPVSAALLSLEQALLPAILPSRPDA | | | | 56919.pro |
| 401 | AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPNDV | | | | MouseGPAT.PRO |
| 401 | AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPDAA | | | | RatGPAT.PRO |
| | 450 | 460 | 470 | 480 | |
| 441 | ADEGRDTSINESRNATDESILRRRLIANLAEHILFTASKSC | | | | 56919.pro |
| 441 | ADEHQDLSINESRNPADEAFRRRLIANLAEHILFTASKSC | | | | MouseGPAT.PRO |
| 441 | AAEHEDMSINESRNADEAFRRRLIANLAEHILFTASKSC | | | | RatGPAT.PRO |
| | 490 | 500 | 510 | 520 | |
| 481 | AIMSTHIVACLLLYRHRQGI DLSTLVEDFFVMKEEVLARD | | | | 56919.pro |
| 481 | AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD | | | | MouseGPAT.PRO |
| 481 | AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD | | | | RatGPAT.PRO |
| | 530 | 540 | 550 | 560 | |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRNDEFFITPS | | | | 56919.pro |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS | | | | MouseGPAT.PRO |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS | | | | RatGPAT.PRO |
| | 570 | 580 | 590 | 600 | |
| 561 | TTVPVSFELNFYSNGVLHV FIMEAIIACSLYAVLNKRGLG | | | | 56919.pro |
| 561 | TTVPVSFELNFYSNGVLHV FIMEAIIACSLYAVLNKRCSG | | | | MouseGPAT.PRO |
| 561 | TTVPVSFELNFYSNGVLHV FIMEAIIACSLYAVQNKRGSG | | | | RatGPAT.PRO |
| | 610 | 620 | 630 | 640 | |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEGTISLPCQTFY | | | | 56919.pro |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEGTISLPCQTFY | | | | MouseGPAT.PRO |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEGTISLPCQTFY | | | | RatGPAT.PRO |
| | 650 | 660 | 670 | 680 | |
| 641 | QVCHETVGKFIQYGILTVAEHDDQEDISPGLAEQQWDDKL | | | | 56919.pro |
| 641 | QVCHETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWDDKL | | | | MouseGPAT.PRO |
| 641 | QVCQETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWNKKL | | | | RatGPAT.PRO |
| | 690 | 700 | 710 | 720 | |
| 681 | PEPLSWSRDEEDEDSDFGEEQRDCYLKVSQSKEHQQTFF | | | | 56919.pro |
| 681 | PE-LNWRSDDEEDEDSDFGEEQRDCYLKVSQSKEHQQTFF | | | | MouseGPAT.PRO |
| 681 | PEPLNWRSDDEEDEDSDFGEEQRDCYLKVSQAKEHQQTFF | | | | RatGPAT.PRO |

FIG. 5C

| | 730 | 740 | 750 | 760 | |
|-----|--------|-------------------|----------------------|---------------|--|
| 721 | LQRL | LGPLLEAYSSAAIFVHN | FSGPVPEPEYLQKLHKYLI | 56919.pro | |
| 721 | LQRL | LGPLLEAYSSAAIFVHN | FSGPVPEPEYLQRLHKYLI | MouseGPAT.PRO | |
| 721 | LQRL | LGPLLEAYSSAAIFVHT | FRGVPVPEPEYLQRLHKYLI | RatGPAT.PRO | |
| | 770 | 780 | 790 | 800 | |
| 761 | TRTERN | VAVYAESATYCLVKN | AVKMFKDIGVFKETKQKRV | 56919.pro | |
| 761 | TRTERN | VAVYAESATYCLVKN | AVKMFKDIGVFKETKQKRV | MouseGPAT.PRO | |
| 761 | TRTERN | VAVYAESATYCLVKN | AVKMFKDIGVFKETKQKRA | RatGPAT.PRO | |
| | 810 | 820 | | | |
| 801 | SVLE | LSSTFLPQCNRQ | KLLEYILSFVVL | 56919.pro | |
| 801 | SVLE | LSSTFLPQCNRQ | KLLEYILSFVVL | MouseGPAT.PRO | |
| 801 | SVLE | LSSTFLPQCNRQ | KLLEYILSFVVL | RatGPAT.PRO | |

FIG.6

Acyltransferase catalytic motif-I

| | |
|------------------|---------------|
| <u>IFLEGTRSR</u> | 56919.pro |
| IFLEGTRSR | MouseGPAT.PRO |
| IFLEGTRSR | RatGPAT.PRO |
| YFVEGGRSR | EcoliGPAT.PRO |

Acyltransferase catalytic motif-II

| | |
|---------------|---------------|
| <u>HRSHID</u> | 56919.pro |
| HRSHID | MouseGPAT.PRO |
| HRSHID | RatGPAT.PRO |
| HRSHMD | EcoliGPAT.PRO |

Acyltransferase catalytic motif-III

| | |
|---------------|---------------|
| <u>ILIIPV</u> | 56919.pro |
| ILVIPV | MouseGPAT.PRO |
| ILVIPV | RatGPAT.PRO |
| ITLIPI | EcoliGPAT.PRO |

Acyltransferase signature motif

| | |
|----------------|---------------|
| <u>GGFFIRR</u> | 56919.pro |
| GGFFIRR | MouseGPAT.PRO |
| GGFFIRR | RatGPAT.PRO |
| GAFFIRR | EcoliGPAT.PRO |

FIG. 7A

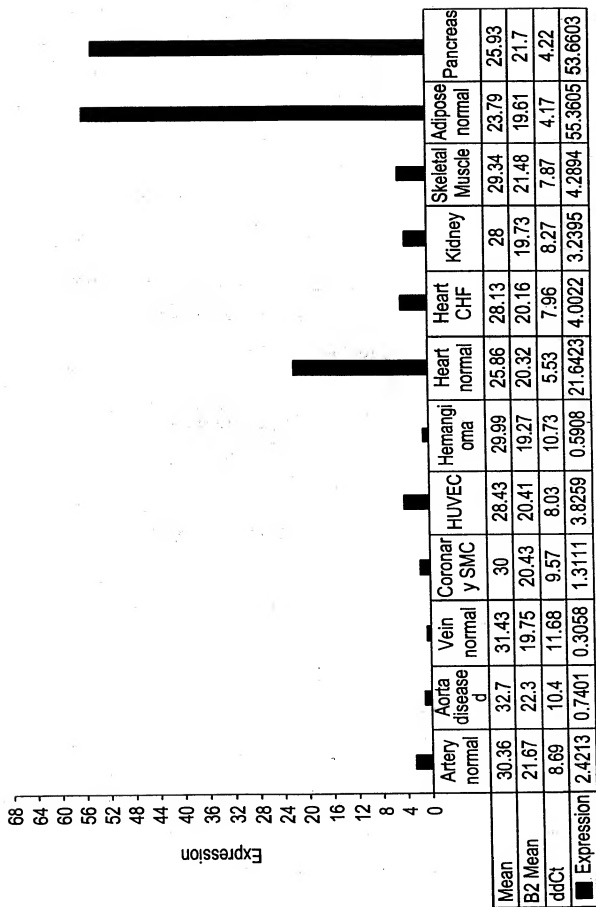


FIG. 7B

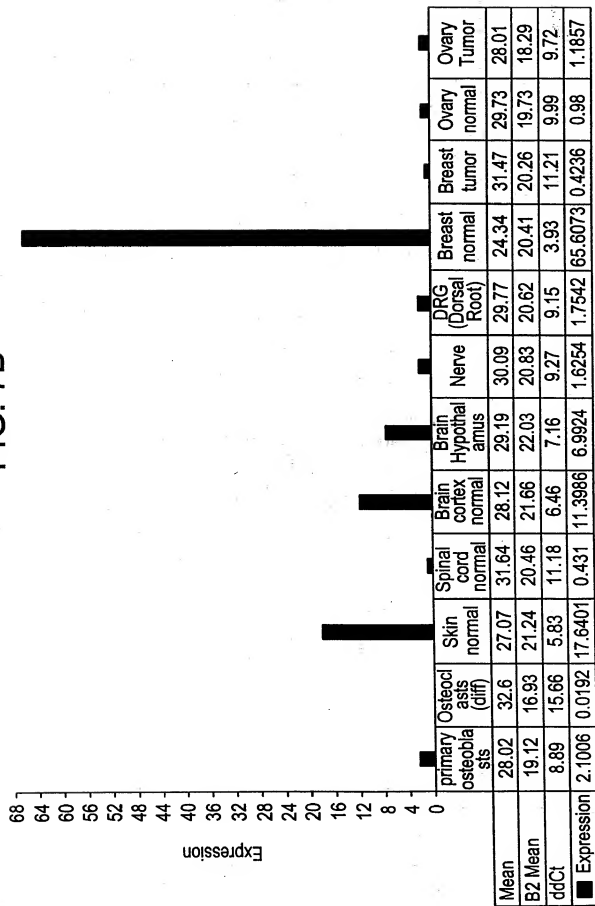


FIG. 7C

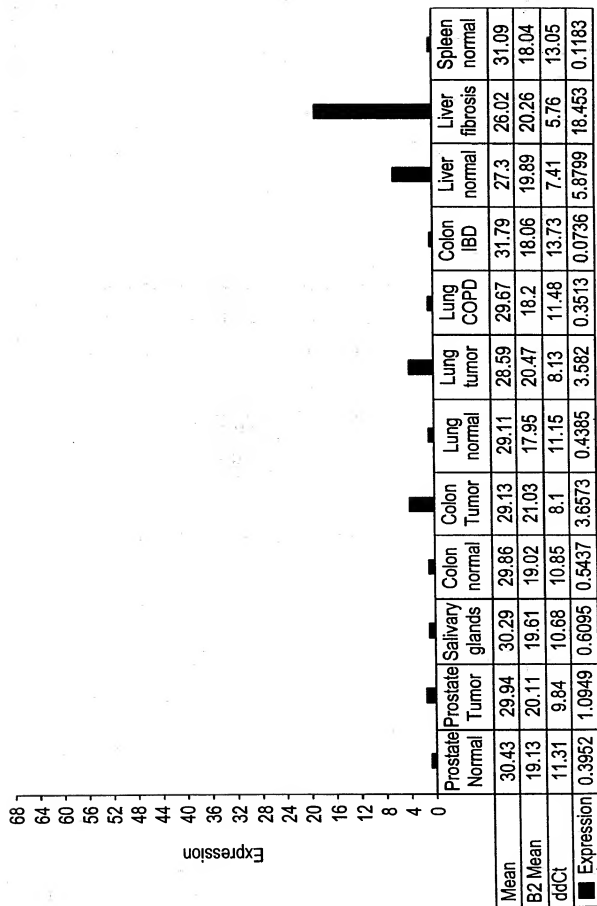


FIG. 7D

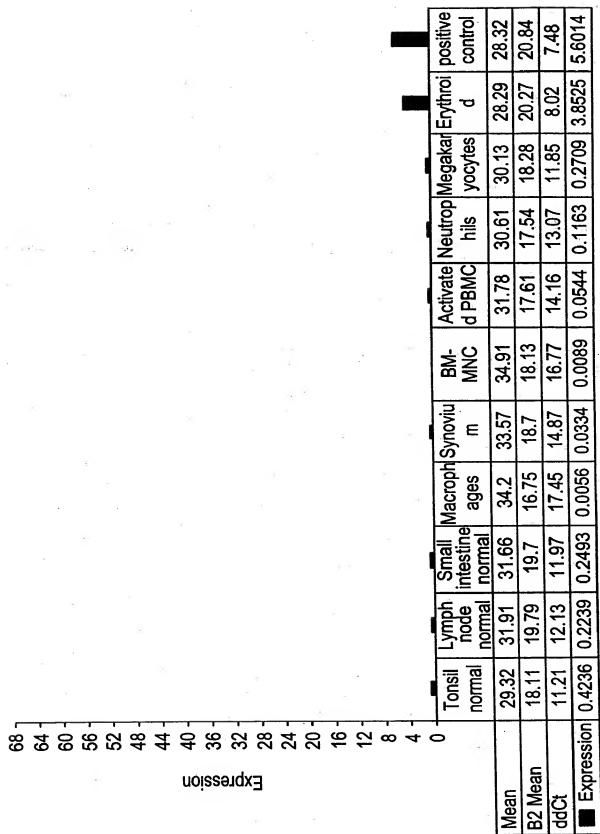


FIG. 8A

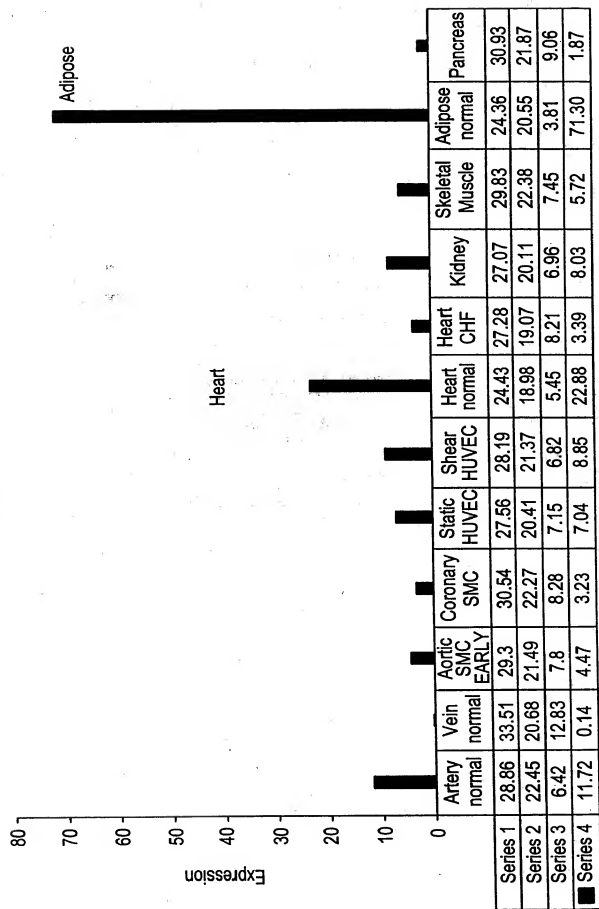
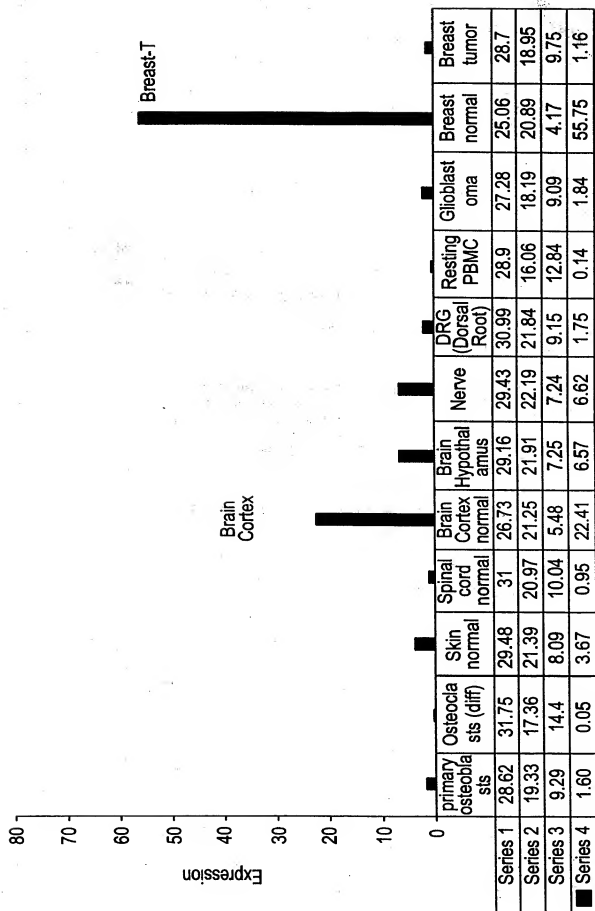


FIG. 8B



Liver

FIG. 8C

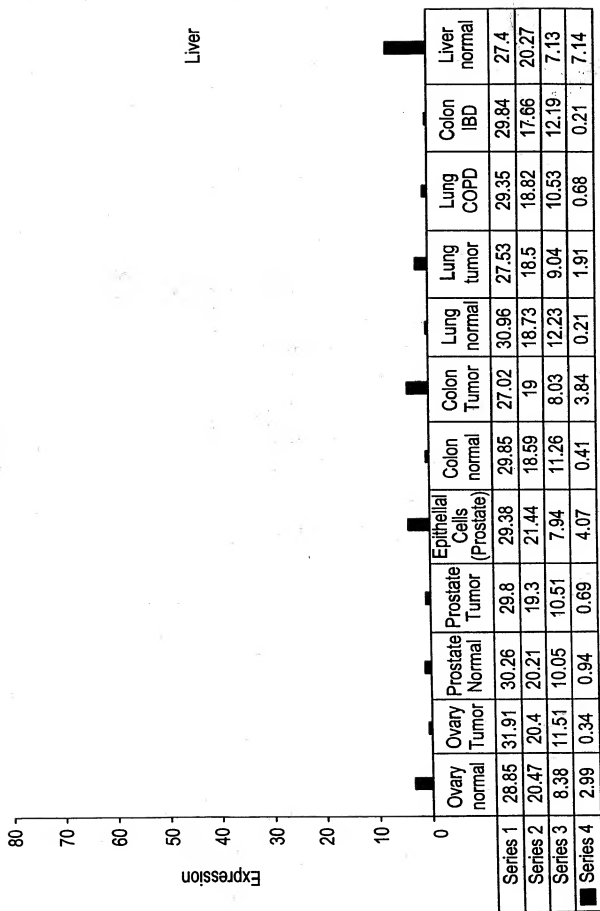


FIG. 8D

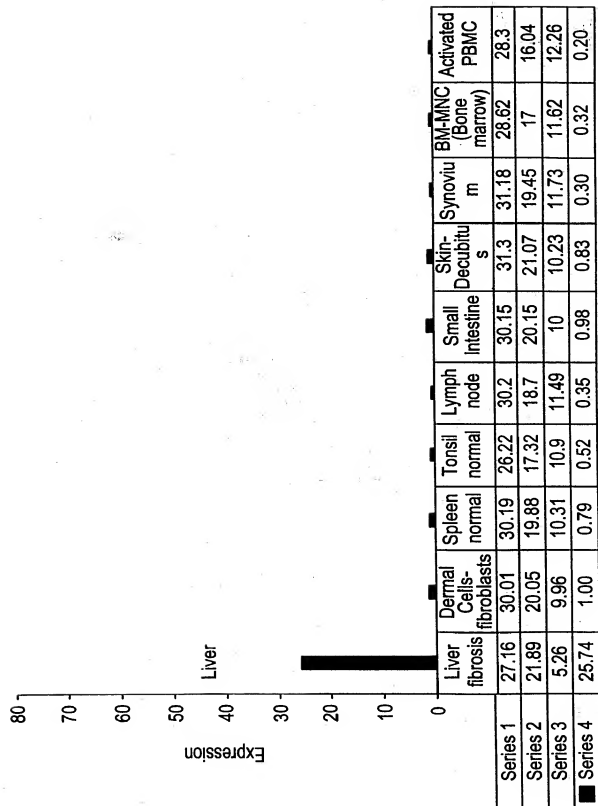


FIG. 9A

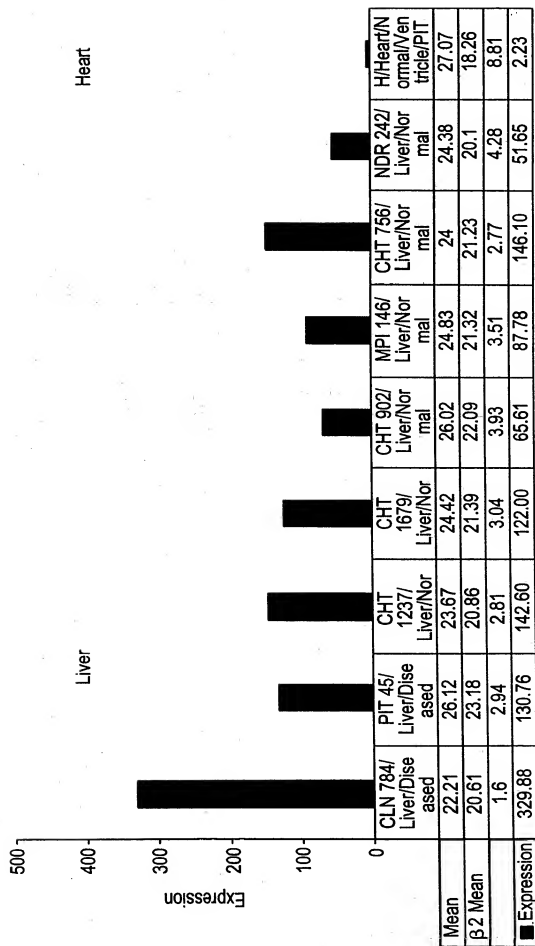


FIG. 9B

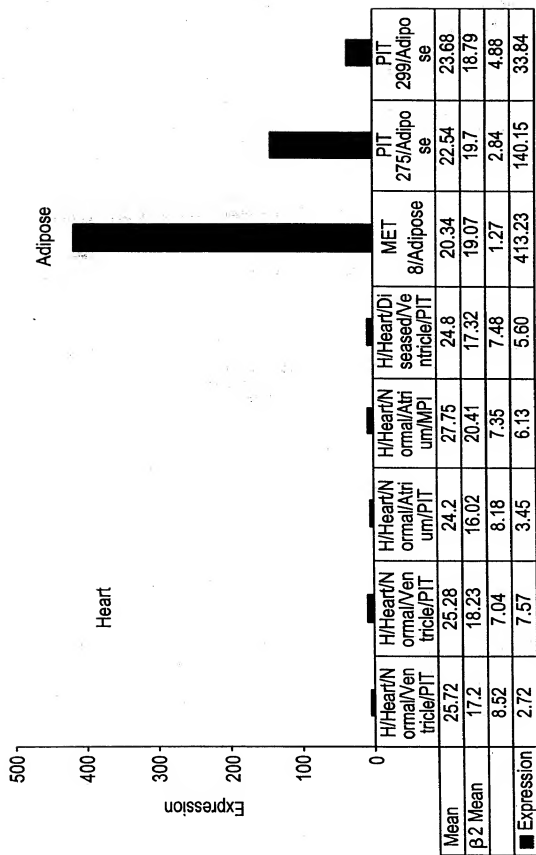


FIG. 10A

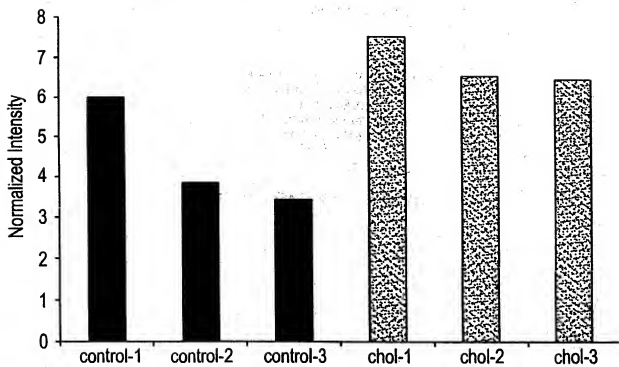


FIG. 10B

